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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=22; hr=12; min=45; sec=12; ms=146; ]

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\*\*\*\*\*

Reviewer Comments:

Leu Glu Phe

30

Tyr Thr Lys Arg Leu Phe Gln Ser Val Ser Pro Ser Phe Leu Ser Ile  
35                          40                          45

Please correct invalid amino acid numbering shown above in sequence id# 48. Please check the remaining sequences for similar errors.

\*\*\*\*\*

Application No: 10785116

Version No: 3.0

**Input Set:****Output Set:**

**Started:** 2009-01-07 15:10:48.392  
**Finished:** 2009-01-07 15:10:52.884  
**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 492 ms  
**Total Warnings:** 33  
**Total Errors:** 9  
**No. of SeqIDs Defined:** 49  
**Actual SeqID Count:** 49

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 201	Mandatory field data missing in <223> in SEQ ID (11)
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
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**Input Set:**

**Output Set:**

**Started:** 2009-01-07 15:10:48.392  
**Finished:** 2009-01-07 15:10:52.884  
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**Total Warnings:** 33  
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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28) This error has occurred more than 20 times, will not be displayed
E 201	Mandatory field data missing in <223> in SEQ ID (45)
E 323	Invalid/missing amino acid numbering SEQID (48) at Protein (35)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (36)
E 323	Invalid/missing amino acid numbering SEQID (48) at Protein (40)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (41)
E 323	Invalid/missing amino acid numbering SEQID (48) at Protein (45)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (46)

SEQUENCE LISTING

<110> Pecker, Iris  
Vlodavsky , Israel  
Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

<130> 27674

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<141> 2004-02-25

<160> 49

<170> PatentIn version 3.1

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1 5

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35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn  
50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe  
100 105 110

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115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp  
130 135 140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe  
145 150 155 160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe  
165 170 175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu  
180 185 190

Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu  
195 200 205

Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn  
210 215 220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser  
225 230 235 240

Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser  
245 250 255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg  
260 265 270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu  
275 280 285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr  
290 295 300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile  
305 310 315 320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly  
325 330 335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala  
340 345 350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys  
355 360 365

Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val  
370 375 380

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro  
385 390 395 400

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405 410 415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg  
420 425 430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly  
435 440 445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu  
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Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu  
465 470 475 480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn  
485 490 495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met  
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Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Leu Met Leu

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20	25	30		
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Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu				
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Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala				
50	55	60		
aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag				299
Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys				
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Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr				
100	105	110		
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Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Glu Asp Ile Cys				
115	120	125		
aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa				491
Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu				
130	135	140		
tgg ccc tac cag gac caa ttg cta ctc cga gaa cac tac cag aaa aag				539
Trp Pro Tyr Gln Glu Gln Leu Leu Arg Glu His Tyr Gln Lys Lys				
145	150	155		
ttc aag aac agc acc tac tca aca agc tct gta gat gtg cta tac act				587
Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr				
160	165	170	175	
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Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu				
180	185	190		
tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc				683
Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu				
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Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly				
225	230	235		

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